derived from image processing of living sepals revealed that while the timing of endoreduplication is central to the pattern of giant cells and small cells, it is insufficient to generate the entire diversity of cell sizes. More live imaging showed that the length of the cell cycle is important for cell size because longer cell cycles give the cell more time to grow. A modified model in which both the timing of endoreduplication and the length of the cell cycle are determined randomly is sufficient to reproduce the distribution of cell sizes in the sepal epidermis. Finally, we further demonstrated that the model could predict the phenotypes of plants with genetically altered cell size patterns. The intertwined and iterative use of modeling combined with biological experimentation allowed us to reach the conclusion that the variability in cell division timing is the mechanism for creating the characteristic and reproducible pattern of cell sizes in the epidermis. The complexity of biology ensures that no model is ever complete, and we are now examining the cellular growth pattern as well as investigating the decision to endoreduplicate at the molecular level.

Modeling plant development with cell complexes in one, two, and three dimensions

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When constructing models of plant development, it is useful to separate consideration of the geometry of a modeled system from its topology. While some changes to a plant during development, such as the elongation of stems or the enlargement of single cells, are purely geometric changes, many developmental changes, such as branching or cell division, modify the system's topology. Therefore, the choice of how to represent the system's topology is an important one. Traditionally, the modeled topology is that of a graph: components, whether functional modules, organs, cells, or abstract subdivisions of cells, are connected to their physical or functional neighbours. However, in physical simulation especially, a more appropriate topology is that of a cell complex. In addition to the components of immediate interest, a cell complex models the connections between them as components, along with the connections between the connections, and so on. For instance, a cell complex model of a three-dimensional multicellular organism models not only the three-dimensional cells, but the two-dimensional cell walls connecting them, the one-dimensional junctions connecting the cell walls, and the zero-dimensional points where cell wall junctions meet. Models of the development of filamentous or branching structures have a one-dimensional connectivity, even if their components are three-dimensional. L-systems provide a well-defined mathematical framework for creating these models, using a graph topology; they can also be used to model these filamentous or branching structures as one-dimensional cell complexes. Significant progress has also been made in extending the ideas of L-systems to the modeling of systems with two-dimensional connectivity, such as cellular layers. The formalisms developed so far, such as vertex-vertex systems, are not (yet) as elegant as L-systems, but they too can represent these systems as two-dimensional cell complexes. However, formal description and modeling of the development of systems with three-dimensional connectivity (such as three-dimensional multicellular structures) has largely remained an open problem. Previous extensions of L-systems to three dimensions rely on developmental rules that are difficult to specify and do not fully capture the topology of the resulting structure. A new modeling framework for three-dimensional cell complexes has been developed. This new framework avoids some of the problems of previous models of three-dimensional plant development by explicitly modeling the entire cell complex. While it is not a direct extension of L-systems to three dimensions, it does extend the idea of the graph rotation system which is so useful in vertex-vertex systems. This provides a useful mechanism for navigating the cell complex structure in a local manner. In this presentation, the ideas behind modeling with cell complexes will be introduced, and some examples of models in one and two dimensions will be shown. The new three-dimensional framework will then be described and demonstrated with a three-dimensional model of the shoot apex of the moss *Physcomitrella patens*.

DigR : how to model root system in its environment? 1 - the model

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Many models already exist through literature dealing with root system representation, among which pure structure models such as Root Typ (Pagès 2004), SimRoot (Lynch 1997), AmapSim (Jourdan 1997); diffusion PDE models (Bastian 2008; Bonneu 2009) and structure/function that are rather scarce and recent (Dupuy 2010)may be aroused. Nevertheless in these studies, root architecture modeling was not carried out at organ level including environmental influence and not designed for integration into a whole plant characterization. We propose here a multidisciplinary study on root system from field observations, architectural analysis, formal and mathematical modeling and finally software simulation. Each speciality is individually investigated through an integrative and coherent approach that leads to a generic model (DigR) and its software simulator that is designed for further integration into a global structure/function plant model. DigR model is based on three main key points: (i) independent root type identification (ii) architectural analysis and modeling of root system at plant level; (iii) root architecture setup indexed on root length. Architecture analysis (Barthelemy 2007) applied to root system (Atger 1994) leads to root type organisation for each species. Roots belonging to a particular type share dynamical and morphological characteristics. Root architectural setup consists in topological features as apical growth, lateral branching, senescence and death, and geometrical features as secondary growth and axes spatial positioning. These features are modeled in DigR through 23 parameters whose values can evolve as a function of length position along the root axes for each root type. Topology rules apical growth speed, delayed growth, death and self pruning probabilities. Branching is characterized by spacing and mixture of lateral root types. Geometry rules root diameter increase, branching

and growth directions (including local deviations and global reorientation). DigR simulator provides a user interface to input parameter values specific to each species. It is integrated into the Xplo environment (Taugourdeau 2010). Its internal multi-scale memory representation is ready for dynamical 3D visualization, statistical analysis and saving to standard formats (MTG(Godin 2007), Obj,). DigR is simulated in a quasi-parallel computing algorithm and may be used either as a standalone application or integrated in other simulation platforms. This will allow further implementation of functional – structural interactions during growth simulation. The software is distributed under free LGPL license and is dedicated both to biologists and modelers. Shown applications (fig. 1) mimic the diversity of root systems and emphasize the genericity of the model according to different sets of parameter values. Examples (fig. 2) prove that additional knowledge may be plugged to DigR to simulate root plasticity facing environmental constraints. Further work will be carried out to apply DigR to various species and to connect DigR to biophysical soil models (Gérard 2008; Zhang et al. 2002); to aerial part models (Barczi 2008); to ecophysiological models (Mathieu 2009, Bornhoffen 2007); and finally to mix this pure descriptive model to a PDE model that handles fine root diffuse modelling (Bonneu 2009).

Sym068: From proplastids to chloroplasts in flowering plants – 26 July

The role of protein transport systems in chloroplast differentiation

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In flowering plants chloroplasts differentiate from proplastids, which are structurally and functionally very reduced organelles in comparison to the photosynthetically active ones. The development of a photosynthetically active chloroplast requires the synthesis and import of a myriad of proteins from the Cytosol and their assembly into functionally active units like the photo systems. Since proplastids contain no or very little internal membrane system thylakoid biogenesis requires also the synthesis of vast amvients of polar lipids to form membrane bilayer prerequisite for protein insertion and complex assembly. Early in chloroplast differentiation the thylakoids are at least in part formed by invagination of the inner envelope membrane. Later, a vesicle transport system seems to take over to replenish thylakoids with pigments, lipids or even proteins. Due to their endosymbiotic origin, plastids still contain their own genome and transcription-translation machinery. All photosynthetic complexes including Rubisco are of dual genetic origin, i.e. subunits are encoded for on the nuclear genome or the plastome. Gen expression, translation, transport and assembly of chloroplast proteins must therefore be coordinated in time, space and quantity to guarantee a sustainable, resource optimized organelle biogenesis. We have identified numerous subunits of the chloroplast protein translocation machinery, named Toc- and Tic-complex. Developmental and organ specific expression of Toc and Tic subunits or their isoforms indicates a rather complex regulatory network in the differential assembly of the translocon units, while the major channel forming proteins Toc75 and Tic110 are required at all plastid developmental stages. Only a few translocon subunits present in primary plastids can also be detected on secondary or complex plastids. Evidence exists for homologues of Tic75, Tic22 and Tic20 even in Apicoplasts of *Plasmodium* and *Toxoplasma*, but also in the ancestors of chloroplasts the cyanobacterial. The evolution of the protein import apparatus was a key event in the endosymbiotic process.

Subcellular and subplastidial proteomics to study intracellular and intraplastidial trafficking of proteins

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Recent advances in the proteomic field have allowed high throughput experiments to be conducted on chloroplast samples. Many proteomic investigations have focused either on the whole chloroplast fractions or on independent suplastidial fractions. However, these previous studies raised the question of the accurate localization of many proteins that were identified in different suplastidial compartments. We recently went a step further into the knowledge of *A. thaliana* chloroplast proteins with regards to their accurate localization within the chloroplast. To achieve this goal, we first obtained highly pure subfractions of envelope, stroma and thylakoids and evaluated their cross-contaminations using biochemical methods. We then performed a comprehensive analysis of the *Arabidopsis thaliana* chloroplast proteome starting from the whole chloroplast and its three main compartments. Then, we assessed the partitioning of each identified protein in the three above-cited compartments using a semi-quantitative proteomic approach and also performed a curated information on envelope proteins (Ferro et al. 2010). An in depth investigation of the proteins identified within the purified envelope fraction allowed new insights over this subplastidial compartment to be revealed (Joyard et al., 2009; Joyard et al., 2010). During the course of this project, we also generated an important tool to investigate the dynamics of the chloroplast proteome at the scale of the whole organelle. This yet unique tool is the first database based on the accurate mass and time tags (AMT) strategy dedicated to plants: the chloroplast AMT database AT-CHLORO (http://www.grenoble.prabi.fr/at_chloro/). This proteomic database was generated in such a way that it can be used for quantitative studies (e.g. comparisons of mutants, impact of adverse growth conditions...). This AMT-based strategy is now used to characterize mechanisms that regulate protein trafficking between the cytosol and the chloroplast, to identify chloroplast proteins that are subjected to these regulatory mechanisms before being imported or during their import into the chloroplast and